

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 24, 1999, 00:40:12 ; Search time 366.45 Seconds
(without alignments)
87.864 Million cell updates/sec

Title: US-09-205-015-1
Perfect score: 9
Sequence: 1 tctgagtca 9

Scoring table: IDENTITY_NUC

Searched: 808301 seqs, 1788773984 residues

Database : GenEmbl.*

- 1: gb_ba1.*
- 2: gb_ba2.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl1.*
- 9: gb_pl2.*
- 10: gb_pr1.*
- 11: gb_pr2.*
- 12: gb_pr3.*
- 13: gb_ro.*
- 14: gb_st.*
- 15: gb_sy.*
- 16: gb_un.*
- 17: gb_vl.*
- 18: gb_htg.*
- 19: em_ba.*
- 20: em_fun.*
- 21: em_hum1.*
- 22: em_hum2.*
- 23: em_in.*
- 24: em_om.*
- 25: em_or.*
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- 27: em_pat.*
- 28: em_ph.*
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- 34: em_htg.*
- 35: em_sts.*
- 36: gb_ba1.*
- 37: gb_ba2.*
- 38: gb_pl1.*
- 39: gb_pl2.*
- 40: gb_pr1.*
- 41: gb_pr2.*
- 42: gb_pr3.*
- 43: gb_sts.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description

C	1	9	100.0	148068	1	AB001488
C	2	9	100.0	24907	1	AB002668
C	3	9	100.0	24907	1	AB002668
C	4	9	100.0	1907	1	AB003186
C	5	9	100.0	1933	1	AB008139
C	6	9	100.0	1950	1	AB008153
C	7	9	100.0	15295	1	AB010150
C	8	9	100.0	2748	1	ACCP5XM
C	9	9	100.0	2878	1	ACMP5EH
C	10	9	100.0	14801	1	AE000688
C	11	9	100.0	15304	1	AE000692
C	12	9	100.0	14150	1	AE000697
C	13	9	100.0	15467	1	AE000723
C	14	9	100.0	16071	1	AE000796
C	15	9	100.0	10932	1	AE000801
C	16	9	100.0	12282	1	AE000818
C	17	9	100.0	10818	1	AE000829
C	18	9	100.0	10865	1	AE000838
C	19	9	100.0	11069	1	AE000850
C	20	9	100.0	10557	1	AE000866
C	21	9	100.0	9938	1	AE000870
C	22	9	100.0	11565	1	AE000874
C	23	9	100.0	10949	1	AE000898
C	24	9	100.0	12694	1	AE000902
C	25	9	100.0	10524	1	AE000906
C	26	9	100.0	12634	1	AE000912
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C	29	9	100.0	15288	1	AE000940
C	30	9	100.0	20434	1	AE000954
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C	34	9	100.0	11103	1	AE001052
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C	36	9	100.0	11703	1	AE001071
C	37	9	100.0	14039	1	AE001107
C	38	9	100.0	3387	1	AF006594
C	39	9	100.0	22060	1	AF008220
C	40	9	100.0	22060	1	AF008220
C	41	9	100.0	2374	1	AF015255
C	42	9	100.0	1254	1	AF023876
C	43	9	100.0	21205	1	AF025396
C	44	9	100.0	87500	1	AF027868
C	45	9	100.0	367	43	G41695

ALIGNMENTS

RESULT 1
AB001488/c
LOCUS
DEFINITION
ACCESSION
NID
KEYWORDS

AB001488 148068 bp DNA
Bacillus subtilis genome sequence, 148 kb sequence of the region
between 35 and 47 degree.
g1881226

21-OCT-1997

BCT

aln: cspC; dlla; dinB; exp2; gslB; mutT; nap; orf8; orf9; orf10;
rsbU; rsbV; rsbW; sigB; sigE; ydaA; ydaB; ydaC; ydaD; ydaE;
ydaF; ydaG; ydaH; ydaI; ydaJ; ydaK; ydaL; ydaM; ydaN; ydaO; ydaP;
ydaQ; ydaR; ydaS; ydaT; ydaU; ydaV; ydaW; ydaX; ydaY; ydaZ;
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ydfY; ydfZ; ydgA; ydgB; ydgC; ydgD; ydgE; ydgF; ydgG;
ydgH; ydgI; ydgJ; ydgK.
Bacillus subtilis (strain:168) DNA.

Eubacteria; Firmicutes; Low G+C gram-positive bacteria;
 Bacillaceae; Bacillus.

REFERENCE
 1 (sites)
 AUTHORS
 Beloin, C., Ayora, S., Exley, R., Hirschbein, L., Ogasawara, N.,
 Kasahara, Y., Alonso, J. C. and Hagarat, F. L.
 TITLE
 Characterization of an lrp-like (lrpC) gene from Bacillus subtilis
 JOURNAL
 Mol. Gen. Genet. 256 (1), 63-71 (1997)
 MEDLINE
 98000887
 REFERENCE
 2 (sites)
 AUTHORS
 Kasahara, Y., Nakai, S., Lee, S., Sadale, Y. and Ogasawara, N.
 TITLE
 A 148 kbp sequence of the region between 35 and 47 degree of the
 Bacillus subtilis genome
 JOURNAL
 Unpublished (1997)
 REFERENCE
 3 (bases 1 to 148068)
 AUTHORS
 Ogasawara, N.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (03-MAR-1997) to the DDBJ/EMBL/GenBank databases. Naotake
 Ogasawara, Nara Institute of Science and Technology, Graduate
 School of Biological Sciences; 8916-5 Takeyama-cho, Ikoma, Nara
 630-01, Japan (E-mail: nogasawa@bs.ist-nara.ac.jp,
 Tel: 07437-2-5430, Fax: 07437-2-5439)

FEATURES
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 /map="35 - 47 degree"

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CDS

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terminator

gene

CDS

RBS

gene

CDS

RBS

gene

CDS


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FFLEKRLSEFMKFTKSLRVFYESIAFGSKFATFGKLEAQFIILVNCILTF
IALMHPQQLFGLISIMVFFGLIPVAGVISLPLISIIAISITGGGMVYLIVLVIFA
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NKEDRSKGPRESNDKK"
35955..35962
/gene-"ydbJ"
35955..36897
/gene-"ydbJ"
35971..36897
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TTLIRIIVGLLKQSGSVTISGFQHDTEFEKAMEAVGAIENPEFYPLTGWNLKHF
ANMKHIDLERVDSVVRVGLTSAIDHKVTYSIGMQRLGIAQAILRHRKLIIDEP
TNGLDPAKGFPROHIRELAEMECTAVLFATHLLREVEDLCDRVIIQKGEIKAEVSL
QCTDOTTETKATIEVQPEKALNWLITGNQYQABSQDGIIVVEAKENIPELNRSILVGD
LNVSITPYTQSLEDEFIKATTAHQEGEEELV"
36906..36912
/gene-"ydbK"
36906..37657
/gene-"ydbK"
36917..37657
/gene-"ydbK"
/note-"PROBABLE MEMBRANE SPANNING PROTEIN."
/codon_start=1
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/db_xref="PID:g1881260"
/translation-"MKLFNRKVTLSLIMAVQFFMALLIKRIVISAGTDENFIGVL

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RBS

gene

CDS

terminator

gene

CDS

RBS

gene

RBS

CDS

gene

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SYTPSLNILQALITIVIAATIVSNEFDKTIKELLIRPVKQKRVFVSKLITVVMVSFY
LYAYVIVALLFGLLFGTSTVATBSKTLVNTLALIGSNWLEAVMMGLFGLGCSLFR
NSAVYVSVFVLYGASTLVQMLKFENKWSFLLFANTDFTQYRSGETALFSGMTPL
FSIGILIIHAIFFIIVGWCCKRDVRV"
37739..37745
/gene-"ydbL"
37739..38087
/gene-"ydbL"
37752..38087
/gene-"ydbL"
/note-"FUNCTION UNKNOWN."
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/db_xref="PID:g1881261"
/translation-"MRNFITALPIVLLGFSVSEMFQFELHVVFRALGLFSLVGLY
MIYKMGIRYFIILYASVIVLAATAFEPIFSFFFGVLGYMTGYLTYMLIYLG
KQDRAHPV"
38204..38210
/gene-"ydbM"
38204..39360
/gene-"ydbM"
38215..39360
/gene-"ydbM"
/note-"SIMILAR TO ACYL-COA DEHYDROGENASE."
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/db_xref="PID:g1881262"
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WDEDYFAVKEVQNGAVINRAATEAKTSGPTGRGREGTHAVKDKGWAVNGRKIFTT
MSQALDYELTAWIEDKQTVGLIHKDDPGLSIEETWDMAMRATSGHDLVNLVEML
DENKIVELQGPRAKPNGLLHPALYLVQAARDYAVQFASEYSPNLSINGIKNV
PAVOQTGEMELELLNARHFLFHIAQLYDDPVRPHLTSELGAAKHITVNAALSVVDK
AMRTVAKSLERTNPQRYRDRAGLHNPMDDAVIHKLAEEAFES"
39362..39386
/note-"PROBABLE RHO-INDEPENDENT TRANSCRIPTIONAL
TERMINATOR"
39385..39577
/gene-"ydbN"
39385..39564
/gene-"ydbN"
/note-"PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN,
SIMILAR TO SENS_BACU."
/codon_start=1
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/db_xref="PID:g1881263"
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IDRKHKNLQENNT"
39571..39577
/gene-"ydbN"
39571..40801
/gene-"ydbO"
39571..39918
/gene-"ydbO"
39571..40801
/gene-"ydbO"
/note-"FUNCTION UNKNOWN, SIMILAR PRODUCT IN B. SUBTILIS
AND E. COLI."
/codon_start=1
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/db_xref="PID:g1881264"
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LNNQDIVASVAVLIGRLISQPADSDHPYHRAETISSLVASFIMAVGTEVLIG
GKAIAGGTETETNLIAATLALGSAVFMGYILYNKRLAASIKSSALMAAKDSRDAF
VSAGAFIGVSSQLKLPWDPVPTAFIIGIITCIITAMDIFKASHSLTDGFHLKDEPY
KQTVGRINVRHKDVKAYLGSVTHIEMVITVDPKLTVEEGHVADEVEDKIRKHEH
VTHVHVHVEPDDIK"
40816..41152
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/gene-"ydbP"

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/ note="PROBABLE THIOREDOXIN."
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/ db_xref="PID:g1881265"
/ translation="MKKITTNEQFNELIQSKEIIVKFYAWDCPDCTRMNMFIDGLE
EYNQNDWELNDELPLDAERYQVMGIPSLIFRNKGTAKHLASNAKTPPEVTEFLS
EHS"
RBS      complement(41143. .41152)
/ gene="ydbp"
/ gene="ydbp"
41311. .42375
/ gene="ddla"
41311. .42375
/ gene="ddla"
/ EC_number="6.3.2.4"
/ codon_start=1
/ transl_table=11
/ product="PROBABLE D-ALANINE--D-ALANINE LIGASE A"
/ db_xref="PID:d1020046"
/ db_xref="PID:g1881266"
/ translation="MYGKSAEHNVSLQALAVIKALNTEKEDIHPITYITEKGEWVRG
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SCEEVEQLGIPCFVKPANLSSVGVISKRNREELQAFELAFQYDRKVVVEERINGR
EIEIGVNDNDPKCSVYGEIAPKTDYDKAKYEDGDTLMPALIVDEEYATISMA
IKAFKIDGSLGRADFFLTADGEVLNEVNTMPGTFPFMSFLLWKEAGVEADLIE
QLVELAKERHAEKOLIKHTF"
42430. .42439
/ gene="ydbp"
42430. .43820
/ gene="ydbp"
42447. .43820
/ gene="ydbp"
/ note="PROBABLE UDP-N-ACETYLURAMYOYLALANYL-D-GLUTAMYL-2,
6-DIAMINOLIGASE (EC 6.3.2.15)."
/ codon_start=1
/ transl_table=11
/ db_xref="PID:d1020047"
/ db_xref="PID:g1881267"
/ translation="MIKRTVKNIAMVKGTLANPOYEQTVIHGVANDTRKLEOHLEFI
PLKGERDGHFVQAEAGVAVLDERSVPNPENHNVILVDDTLALQOLAKATIQ
ELGTRVIGTVSGNKTITKMIHVLGTQIRVHTGGNNHNGHGLPULVAMPENTEI
AVLEMSGAKEIDLLSKLANPDAVITNIGESMODLGRREGIAEAKLEIINGLED
GLYIYIDEPILQWAYSCOTKTYGTGTYNDYQODVSQSEGTHTIKGIENTFFPI
LGRNVNMAAIAAGAYFGIAPEDAAGLSGLKVTGMRLIKTDSGLSIINDATNA
SPTSMKAAIOLTESLEGYGGKMLVLGDMLEGLDETFHEKCGNAVSPDKIDRVFTYG
KLGAFLAEGALKHEKDRVSHYTEKDKLLQAVKENASKGLDILFKASRGMKLEEIVND
LIESPLS"
44152. .45704
/ gene="ydbp"
44152. .44157
/ gene="ydbp"
44169. .45704
/ gene="ydbp"
/ note="ATP-DEPENDENT RNA HELICASE DEAD HOMOLOG."
/ codon_start=1
/ transl_table=11
/ db_xref="PID:d1020048"
/ db_xref="PID:g1881268"
/ translation="MVNHDITETAIRSLNNLITTFODFNLSDDLKAINRMGFEPAT
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QVSELYIKGDKRAKVLPIYQDQIGSLRNKKNPNIIVGTPGRLLDHNRTIRL
NNVNTVMDADEMLNMGFIDDIIESLNVPSHQTLLFSATWPAFKTRAEFMTEP
EHRVKGAAEHSVNIQOYLEVOERKEDTLRLDIQSPELAIYFGRKRVDELAEL
ALNLRGYAEGIHGDLQAKEMVALRKFEAGAEVLVAIDVAAGLDISGVTHVIND
VPQDESIVHRIGTRGAKTGMAWTFITPREKSMRLAIQTTRKMRKKEPTLDEA
LEGQQQVETRTTISENNLNFYMTAAELLEHDVATVYAAAIKMAIKPEPDPTVR
LTDEAPVMSKRYKNQRSKRDRDGGGGRGGKGNRNRSSYDKKRNDRRSSGDRQK
KSY"
45720. .45748
/ note="PROBABLE RHO-INDEPENDENT TRANSCRIPTIONAL
terminator

TERMINATOR"
45859. .45868
/ gene="ydbp"
45859. .46356
/ gene="ydbp"
45877. .46356
/ gene="ydbp"
/ note="FUNCTION UNKNOWN."
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/ db_xref="PID:d1020049"
/ db_xref="PID:g1881269"
/ translation="NREQPKNQISPDGLKVMRLQELIISAVCLLIVIAVAVLSYFFHW
VOHISGLGAVMLLSIVTVFTIPKVRHKVWRYEVEHEIDIOSGIFVTVRVIPVMVR
YHVDTSGPLLLKYNLATVKTSTAATVHSIPALEMEADRLRDSISRLARVTDVV"
46332. .46339
/ gene="ydbp"
46332. .47827
/ gene="ydbp"
46346. .47827
/ gene="ydbp"
/ note="FUNCTION UNKNOWN."
/ codon_start=1
/ transl_table=11
/ db_xref="PID:d1020050"
/ db_xref="PID:g1881270"
/ translation="MMSBPKRLHPVAVILNCHTIIQIKNILLPFFFFVIVNSNHTV
RYGALAGVLFILWVAASIIKWRFTRYIEDDERIEGLEFVTKKRIISIDRIQTMN
EERLEAEELDPSVEQHEIRNMARELLMAASTGGIGVIIISAVFALISQDLDEPLMD
WLFQSFLOHASIGIYAVLIFIGLFIWIFSIAGMFRYANFQIKKEQELIVSRGI
IEKHQVTIPLRKIQAIKENIIROLFQFVTVSVSAGSGDREKEGALTILFPMIHK
KKLPHMLRTFTEVLTENCRRLPRALKRVLFERSVIFSLIILPLCIFQPGYLSV
ILLPIELFGYLAYKEAANTINGDRLQITRFIGRTAIVLKKRMQVCKFSQSIFQAK
GRLYTISVSKSSSHEELTVDVGEADAFLKWTYSYKADG"
complement(48079. .48691)
/ gene="ydcA"
/ gene="ydcA"
/ note="FUNCTION UNKNOWN, SIMILAR PRODUCT IN H. INFLUENZAE
AND SYNCHOCYSTIS."
/ codon_start=1
/ transl_table=11
/ db_xref="PID:d1020051"
/ db_xref="PID:g1881271"
/ translation="MFIETNEQFIRLYPVVTFILALQAVLWLFPSLPAHSVILWRD
TVYGNLVANGAEWRLLTPLLHAGFTHLLFNMSIFLPAPALERMGLKARFLLVYA
GSGIIGNIGTYIETPLDVHVAGSAGIPLGFLGVLFVLFVFRNELIGQESHKMITLLA
FAYLMSFINSNNMNAHLFGLCGGFLSLFCVQKKERY"
complement(48685. .48691)
/ gene="ydcA"
48756. .48764
/ gene="ydcB"
48756. .49138
/ gene="ydcB"
48773. .49138
/ gene="ydcB"
/ note="FUNCTION UNKNOWN, SIMILAR PRODUCT IN E. COLI AND
MYCOPLASMA PNEUMONIAE."
/ codon_start=1
/ transl_table=11
/ db_xref="PID:d1020052"
/ db_xref="PID:g1881272"
/ translation="MIVGIGLDITELKRIASWAGKQKFAEIRLTRSELDOYIELSEK
RKNELFARPAKFAFSGTGTGRLSGQSLFODIETRKDQNGKPYIITCKLSQAAPHVS
IHTHKEYAAAQVVERLSS"
49183. .50320
/ gene="ydcC"
49183. .49189
/ gene="ydcC"
49199. .50320
/ gene="ydcC"
/ note="FUNCTION UNKNOWN."
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WHKPSLYRYLENPKKQKQOVILRNENGVFVLTSLNKSFRFQSDMPNNSQVYLF
SLKVDQNDSDAVFTAKKRYVFTETKTYNQHNKMLPTQETTFNKDKMSPSSVYVMDTD
KVMVKVFSSEFFENKQFDEKSEDEKKNMTLSQMDVATSAKPSDTPFAVKTPIELPLGV
KLEEKDISTEDCKRIIMTYGGEKSTLQEKAKIAKASSVTLNGEPVNLGVTIGAL
SDASLSWTYGVGYLLSSKDLSEEMVTVAKSQGQSSK"
50326..50354
/terminator
/feature="PROBABLE RHO-INDEPENDENT TRANSCRIPTIONAL
TERMINATOR"
50422..51604
/gene="alr"
50422..50429
/gene="alr"
50435..51604
/gene="alr"
/EC_number="5.1.1.1"
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/product="ALANINE RACEMASE"
/db_xref="PID:d1020054"
/db_xref="PID:g1881274"
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YHGDAFTAALADAGACLAVALIDEAISLRKKGLKAPILVLGAVPPEVVAIAAEYD
VTLGYSVENLQEAARHTKKGSLEHLKVDTGMNRLGVKTEEVQNVMAILLORNPLK
CKGVTFHFADEKERYFLMQFERFKELIAPLPLKNLVHCANSAAGLRLLKGFENA
VRFGIYGVLADGWSLDEIPFQLRPAFTLHSLVKLIRKGESVSYGAETKATKTD
WIGTVPYVAGDWLRKLKGTDLVKGRLKRIAGRICMDQPMVELDQEPYGPYKVTILG
ROGEVYSMEIEIAGLETINYEACTISSRVPVRFLENGSIMEVRNPLQLQVNISN"
51705..52001
/gene="ydcB"
51705..51711
/gene="ydcB"
51720..52001
/gene="ydcB"
/feature="FUNCTION UNKNOWN."
/codon_start=1
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/db_xref="PID:g1881275"
/transl_table="MSESSARTENKMSLISLVAELDGVAMREKRSRNELISQAVRAY
VSERTTRHNRDLMRGVMEMAKINLINSSEAHFAECEATTVERLVSGG"
51993..52356
/gene="ydcE"
51993..51997
/gene="ydcE"
52006..52356
/gene="ydcE"
/feature="FUNCTION UNKNOWN, SIMILAR PRODUCT IN MYCOBACTERIUM
TUBERCULOSIS AND STAPHYLOCOCCUS AUREUS."
/codon_start=1
/transl_table=11
/db_xref="PID:d1020056"
/db_xref="PID:g1881276"
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AAITAOIQAKLPTHVEIDAKRYGFERDSVILQIINTDKRLTKITHLDEMDMK
VDEALQISLALIDF"
52369..52394
/terminator
/feature="PROBABLE RHO-INDEPENDENT TRANSCRIPTIONAL
TERMINATOR"
52457..52462
/gene="orfB"
52457..53295
/gene="orfB"
52471..53295
/gene="orfB"
/feature="FUNCTION UNKNOWN."
/codon_start=1
/transl_table=11

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TLPQESTELLWOIDREFPNSIEFNOQYSISWEKTYSLQKIALQELSAKLPVFEENI
RVMPLEGTIDTERAKRMENLNGVVAHRQSVLLIDITGVVVDIMVAHHIIOASEAV
RLVAKGALLAGIRPEIAQTIVNLGIDLSQVITTKNTLQKGIQTALQEMTDKRVISLGE"
53286..53290
/gene="orfS"
53286..53665
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53300..53665
/gene="orfS"
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/db_xref="PID:g1881278"
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ETALDLQGLTAKRELGE"
53656..54070
/gene="orfM"
53656..53660
/gene="orfM"
53669..54070
/gene="orfM"
/codon_start=1
/transl_table=11
/product="SIGMA-B REGULATOR"
/db_xref="PID:d1020059"
/db_xref="PID:g1881279"
/transl_table="MNDQSCVRIEMTDIIVAAROLGRNVAKELGFTVDOARITTAIS
ELARNIYLAGQIGIEQVADRKGKGLKIAEDQPGPIPIRKVMEDGFTSGGLGA
GLPGVKRLMDESLNSVAGEETEIAIKWLK"
54089..55089
/gene="rsbU"
54069..54075
/gene="rsbU"
54082..55089
/gene="rsbU"
/feature="SIMILAR PRODUCT IN SYNECHOCYSTIS."
/codon_start=1
/transl_table=11
/product="SIGMA FACTOR SIGB REGULATION PROTEIN RSBU"
/db_xref="PID:d1020060"
/db_xref="PID:g1881280"
/transl_table="MDFREVLQEVHOLLSRYIAELTETSILYQAQFSRKTIEHQIPP
BEIISHRKVLKELYPSLPEDYFHSLSDFLEIWMIGYGMAYQEHTLRGICQEKSEIE
IAANVQTLTGKVPQEEALDIGAISVPAKQMSGDYTHFVKDKESINIAIADVIGKI
PAALCMSIKYAMDLSLPTGTHPSQVLKLNRYVEQNVDSMFTIMFIANYNMDKHQF
TYASAGHPGPFYYSQKNTFYDLEAKGLVIGISQDYDKQFDQHLKRGDMIVLFSQGV
TECRTENGFLERPDQLKLEIEMCMSSAQEMVKNIYDSLLKLQDFQLHDDFTLIVLRK
V"
55139..55480
/gene="rsbV"
55139..55145
/gene="rsbV"
55151..55480
/gene="rsbV"
/feature="SIMILAR PRODUCT IN SYNECHOCYSTIS."
/codon_start=1
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/db_xref="PID:d1020061"
/db_xref="PID:g1881281"
/transl_table="MNINVDYKQENDIQVNIAGEIDVYSAPVLREKLVPLAEQADL
RICLADSVISMDSTGLGVFGVTFKMKVKKGGSLKENLSERLIRLFTITGLKDIIDISA
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55462..55959
/gene="rsbW"
55462..55469
/gene="rsbW"

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CDS      55477..55959
/gene="rsb"
/codon_start=1
/transl_table=11
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RBSW)"
/db_xref="PID:d1020062"
/db_xref="PID:g1881282"
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IAYSEACTNVAQHAYEDKNGEYSIRFGFEDLEIVADGSDFDQKQDGLGPT
PSHTVDQSGGLGLYMETLMDEVYQNHSGVTVAMTYLNGERVDHDTTKNETH"
gene      55909..56713
/gene="sig"
RBS      55909..55914
/gene="sig"
CDS      55919..56713
/gene="sig"
/codon_start=1
/transl_table=11
/product="RNA POLYMERASE SIGMA-B FACTOR (SIGMA-37)"
/db_xref="PID:d1020063"
/db_xref="PID:g1881283"
/transl_table="MIMTOPSKTKTKDEVDRLISDYOTKODEQAQETLVRYTNLV
DLAKYKSGKSFHDLROVMIGLIGALKRYPVVGKSFEEAFIPTIIGEKRLRD
KTVSHVPRIKELPRIKAMVDLTETQSPKVEIEAEFLDVEEVEIETWEMGRS
YQALSDHSTEADSDGSTVITLDIVGSDQEDYERNQOLQSLVLSHSDREKQIDIL
TYIONKSQKETGDLIGISOMHVSRLQKAVKRLREALIEDPSNMLM"
RBS      56699..56705
/gene="rsb"
gene      56699..57312
/gene="rbx"
CDS      56713..57312
/gene="rbx"
/codon_start=1
/transl_table=11
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REGION)"
/db_xref="PID:d1020064"
/db_xref="PID:g1881284"
/transl_table="MIQVEENHEIOTLVQLNKEGKSGICGDSFFMKADDKELICAVD
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TYCSGVNFIHLSPSGESFYPLPISGLSGPKQKHTATAYEKGSKIHTDGLNV
PDIRSLHKGQSVVEEISLSLKMVTSRKDDLIYLGOLS"
terminator 57321..57353
/note="PROBABLE RHO-INDEPENDENT TRANSCRIPTIONAL
TERMINATOR"
gene      57539..57848
/gene="ydcf"
RBS      57539..57544
/gene="ydcf"
CDS      57555..57848
/gene="ydcf"
/note="FUNCTION UNKNOWN."
/codon_start=1
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/db_xref="PID:g1881285"
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VLQKQKEDICITYGIVLEGAEAKWGEIIGTSLSKDMPATVSRVLHYLYGVK"
RBS      57833..57840
/gene="ydcg"
gene      57833..58285
/gene="ydcg"
CDS      57845..58285
/gene="ydcg"
/note="FUNCTION UNKNOWN, SIMILAR PRODUCT IN BACILLUS
LICHENIFORMIS."
/codon_start=1
/transl_table=11
/db_xref="PID:d1020066"
/db_xref="PID:g1881286"
/transl_table="MNTNYIGWSEQHVLKGAAGGFAQLCHGKAPLAKKKEGDWLI
terminator 61137..61165
/note="PROBABLE RHO-INDEPENDENT TRANSCRIPTIONAL
TERMINATOR"
gene      61351..61817
/gene="ydcf"
RBS      61351..61360
/gene="ydcf"
CDS      61365..61817
/gene="ydcf"
/note="FUNCTION UNKNOWN."
/codon_start=1
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/db_xref="PID:d1020070"
/db_xref="PID:g1881290"
/transl_table="MDNKELOKLTDEISYFKKPFERHOALFNDRLKTTGGVLLTSH
NIELNRKYLIEHGRELIGLIKHELCHYHLHGKGYKHDRDFMLLOQVNAFPRECT
PLAKKAENKTYMVICITTCGQYIKRAMNPDYRCGKCGKIKRIFS"
61940..62014
/product="trna-Asn"

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YSPRDAYPDGKLLRSFTAIGKVKSGNIYPYOMAPNFIPIYRLDIDYVPCHKIGFYDIK
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58253..58260
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58253..58712
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58269..58712
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/note="FUNCTION UNKNOWN."
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LITCKYMAHGETVTOKKLASFOTNIMMVSEVVRLEKKGFIERSKNPQDKREVLL
SLTEIGGEKVTAALPIVEKIDQAFPAAMKKNELSLQLELLKHE"
58791..58795
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CDS       65528..65788
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RKSDFGSGFDLSDGTTGTTIVFGSKSEAYLCFYEKNEQAEKYNIPLELGDWRY
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70205..70210
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70212..71285
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Query Match      100.0%; Score 9; DB 1; Length 148068;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9
    |||||
Db 119312 TCTGAGTCA 119304

RESULT 2
AB002668      24907 bp      DNA      BCT      21-FEB-1998
LOCUS      Actinobacillus actinomycetemcomitans DNA for glycosyltransferase,
DEFINITION      lytic transglycosylase, dTDP-4-rhamnose reductase, complete cds.
ACCESSION      AB002668
NID      g1944153
KEYWORDS      rhamnosyltrasferase; glycosyltransferase; exonuclease III;
galactosyltransferase; rhamnosyltransferase; ABC transport protein;
dTDP-4-keto-6-deoxy-D-glucose-3,5-epimerase; dTDP-4-rhamnose
reductase; glucose-1-phosphate-thymidyltransferase e;
dTDP-D-glucose-4,6-dehydratase; lytic transglycosylase.
SOURCE      Actinobacillus actinomycetemcomitans (strain:Y4) DNA.
ORGANISM      Actinobacillus actinomycetemcomitans
Eubacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Actinobacillus.
REFERENCE      1 (sites)
AUTHORS      Yoshida,Y., Nakano,Y., Yamashita,Y. and Koga,T.
TITLE      Identification of a genetic locus essential for serotype b-specific
antigen synthesis in Actinobacillus actinomycetemcomitans
JOURNAL      Infect. Immun. 66 (1), 107-114 (1998)
MEDLINE      98084462
REFERENCE      2 (bases 1 to 24907)
AUTHORS      Yoshida,Y.
TITLE      Direct Submission
JOURNAL      Submitted (07-APR-1997) to the DDBJ/EMBL/GenBank databases. Yasuo
Yoshida, Kyushu University Faculty of Dentistry, Department of
Preventive Dentistry; 3-1-1 Maidashi, Higashi-Ku, Fukuoka, Fukuoka
812-82, Japan (E-mail: yasuo@haembox.nc.kyushu-u.ac.jp,
Tel:092-642-6423, Fax:092-642-6354)
FEATURES
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BASE COUNT 7539 a 4293 c 5099 g 7976 t
ORIGIN

Query Match 100.0% Score 9; DB 1; Length 24907;

Best Local Similarity 100.0%; Pred. No. 4.5e+03; Mismatches 0; Indels 0; Gaps 0;
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QY 1 tctgagtca 9

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Db 3342 TCTGAGTCA 3350

RESULT 3

AB002668/c

LOCUS

AB002668 24907 bp DNA BCT 21-FEB-1998
Actinobacillus actinomycetemcomitans DNA for glycosyltransferase,
lytic transglycosylase, dTDP-4-rhamnose reductase, complete cds.

ACCESSION

AB002668

NID

KEYWORDS

g1944153
rhamnosyltransferase; glycosyltransferase; exonuclease III;
galactosyltransferase; rhamnosyltransferase; ABC transport protein;
dTDP-4-keto-6-deoxy-D-glucose-3,5-epimerase; dTDP-4-rhamnose
reductase; glucose-1-phosphate-thymidyltransferase e;
dTDP-D-glucose-4,6-dehydratase; lytic transglycosylase.
Actinobacillus actinomycetemcomitans (strain:Y4) DNA.

SOURCE

ORGANISM

Actinobacillus actinomycetemcomitans
Eubacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Actinobacillus.

REFERENCE

1 (sites)

Yoshida,Y., Nakano,Y., Yamashita,Y. and Koga,T.

TITLE

Identification of a genetic locus essential for serotype b-specific
antigen synthesis in Actinobacillus actinomycetemcomitans

JOURNAL

Infect. Immun. 66 (1), 107-114 (1998)

MEDLINE

9808462

REFERENCE

2 (bases 1 to 24907)

Yoshida,Y.

TITLE

JOURNAL

Direct Submission

Submitted (07-APR-1997) to the DDBJ/EMBL/GenBank databases. Yasuo
Yoshida, Kyushu University Faculty of Dentistry, Department of
Preventive Dentistry; 3-1-1 Maidashi, Higashi-ku, Fukuoka, Fukuoka
812-82, Japan (E-mail: yasuo@haemobox.nc.kyushu-u.ac.jp,
Tel:092-642-6423, Fax:092-642-6354)

FEATURES

source

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tctgagtcg 9
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DB 13553 TCTGAGTCA 13545

RESULT 4
AB003186/c
LOCUS
DEFINITION
AB003186
complete cds.
ACCESSION
NID
2055257
KEYWORDS
Polyhydroxybutyrate depolymerase
SOURCE
Comamonas acidovorans (strain:YML1609) DNA.
ORGANISM
Comamonas acidovorans
REFERENCE
1 (sites)
Eubacteria; Proteobacteria; beta subdivision; Comamonas.
AUTHORS
Kasuya,K., Inoue,Y., Tanaka,T., Akehata,T., Iwata,T., Fukui,T. and
DOI,Y.
TITLE
Biochemical and molecular characterization of the
polyhydroxybutyrate depolymerase of Comamonas acidovorans YML1609,
isolated from freshwater
Appl. Environ. Microbiol. 63 (12), 4844-4852 (1997)
JOURNAL
MEDLINE
98069478
REFERENCE
2 (bases 1 to 1907)
Kasuya,K.
Direct Submission
Submitted (18-APR-1997) to the DDBJ/EMBL/GenBank databases.
Ken-ichi Kasuya, The Institute of Physical and Chemical Research
(RIKEN), Polymer Chemistry Lab.; Hirosawa 2-1, Wako, Saitama
351-01, Japan (E-mail:kkasuya@postman.riken.go.jp.
Tel.048-462-1111, Fax:048-462-4667)
LOCATION/Qualifiers
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Query Match 100.0%; Score 9; DB 1; Length 1907;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1662 TCTGAGTCA 1654

RESULT' 5
LOCUS AB008139/c
DEFINITION Enterobacter gergoviae gene for GroES protein homolog, GroEL protein
          homolog, partial cds.
ACCESSION AB008139
NID 92980903
KEYWORDS GroES protein homolog; GroEL protein homolog.
SOURCE Enterobacter gergoviae (strain:JCM 1234) DNA.
ORGANISM Enterobacter; Proteobacteria; gamma subdivision; Enterobacteriaceae;
          Enterobacter.
REFERENCE 1 (sites)
AUTHORS Harada,H. and Ishikawa,H.
TITLE Phylogenetical relationship based on groE genes among
phenotypically related Enterobacter, Pantoea, Klebsiella, Serratia,
and Erwinia species
JOURNAL J. Gen. Appl. Microbiol. 43, 355-361 (1997)
REFERENCE 2 (bases 1 to 1933)
AUTHORS Harada,H.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-1997) to the DDBJ/EMBL/GenBank databases. Hosami
of Biological Sciences; Hongo, Bunkyo-ku, Tokyo 113, Japan,
Bunkyo-ku, Tokyo 113, Japan (E-mail:hosami@biol.s.u-tokyo.ac.jp,
Tel:03-3812-2111, Fax:03-3816-1965)
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Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1662 TCTGAGTCA 1654

RESULT' 6
LOCUS AB008153/c
DEFINITION Erwinia aphidicola gene for GroES protein homolog, GroEL protein
          homologue, partial cds.
ACCESSION AB008153
NID 92980945
KEYWORDS GroES protein homolog; GroEL protein homolog.
SOURCE Erwinia aphidicola (strain:IAMI4479) DNA.
ORGANISM Erwinia; Proteobacteria; gamma subdivision; Enterobacteriaceae;
          Erwinia.
REFERENCE 1 (sites)
AUTHORS Harada,H. and Ishikawa,H.
TITLE Phylogenetical relationship based on groE genes among
phenotypically related Enterobacter, Pantoea, Klebsiella, Serratia,
and Erwinia species
JOURNAL J. Gen. Appl. Microbiol. 43, 355-361 (1997)
REFERENCE 2 (bases 1 to 1950)
AUTHORS Harada,H.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-1997) to the DDBJ/EMBL/GenBank databases. Hosami
of Biological Sciences; Hongo, Bunkyo-ku, Tokyo 113, Japan,
Bunkyo-ku, Tokyo 113, Japan (E-mail:hosami@biol.s.u-tokyo.ac.jp,
Tel:03-3812-2111, Fax:03-3816-1965)
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Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctgagtcga 9
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Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 7480 TCTGAGTCA 7488
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RESULT 8
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LOCUS A.calcoaceteticus epsx and epsm genes.
DEFINITION X81320
ACCESSION 9559387
NID epsx; epsm; GDP-mannose pyrophosphorylase; phosphomannose
isomerase.
SOURCE Acinetobacter calcoaceteticus.
ORGANISM Acinetobacter calcoaceteticus
Eubacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
Acinetobacter.
REFERENCE 1 (bases 1 to 2748)
AUTHORS Stark, M. and Kaplan, N.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2748)
AUTHORS Stark, M.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-1994) M. Stark, Tel Aviv University, Dept of
Molecular Microbiology & Biotechnology, Ramat-Aviv, 69978 Tel-Aviv,
ISRAEL

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QQAQSDTLMVLADADHYITTEQDKFEQSIQALAKLDLVTGIVTHAETGYVI
EKGNSELNGFQVRFVEPAPATAQEYLESQFLMNSANFMFKADIVILNEIQQHAQDI
YNSCSAMQDTKADLDIFRIDKEAFKQCRSESDIYANMEOTKDAVVPVLDANWDS
WSALWDIQDKDQGNVIQGDVITVKSQNNYVFSRSLVSLGLVDNVLVIETKDALVA
DKSKVQDIKKIVESIKEQGRTEHFCHREVYRPWGKYSIDHAERYQVKRITVTPKQKL
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SIQHHRSSEHWVNGTAKIHKGKESFLLTENQSTYIPLGEIHALENPGKVPLELIE
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 BASE COUNT 825 a 506 c 516 g 901 t
 ORIGIN

Query Match 100.0%; Score 9; DB 1; Length 2748;

Best Local Similarity 100.0%; Pred. No. 6.2e+03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctgagtcga 9
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 Db 1793 TCTGAGTCA 1785

RESULT 9

ACIMPDEH ACIMPDEH 2878 bp DNA BCT 01-SEP-1992
 LOCUS A.calcoaceticus gene for inosin-5-monophosphate dehydrogenase and a
 DEFINITION putative ferredoxin.
 ACCESSION X68859
 NID 938718

KEYWORDS ferredoxin; inosine-5'-monophosphate dehydrogenase.
 SOURCE Acinetobacter calcoaceticus.
 ORGANISM Acinetobacter calcoaceticus
 Eubacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
 Acinetobacter.

REFERENCE 1 (bases 1 to 2878)

Anderegg,U.

Direct Submission

TITLE Submitted (11-JUN-1992) U. Anderegg, Univ. Leipzig, Fach.

JOURNAL Biowissenschaften, Talstrasse 33, 0-7010 Leipzig, FRG

REFERENCE 2 (bases 1 to 2878)

Anderegg,U., Schunck,W.H., Asperger,O. and Kleber,H.P.

JOURNAL Unpublished

FEATURES Location/Qualifiers

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/organism="Acinetobacter calcoaceticus"

/strain="EB 104"

/db_xref="taxon:471"

/clone="pUC 119-64"

252..617

/codon_start=1

/transl_table=11

/product="ferredoxin (putative)"

/db_xref="PID:g38719"

/db_xref="SWISS-PROT:P31004"

/translation="MLSVATPDECLRCACCAHFRVSFYWAEAELEHVEPLTPV

YSCMRGTNQPFCRCALTGEIGKEVGCSTYAVRSSTCREVQIADQCNRKLAHQIPL

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753..2219

/EC_number="1.1.1.205"

/codon_start=1

/transl_table=11

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/db_xref="PID:g38720"

/db_xref="SWISS-PROT:P31002"

/translation="MLTIQVEALTDEDDVLLPAYSTVLPKOVSLKTRITRGIYLNPL

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VREGESKNIQALLQKRIEYKLVVYGESNELGLITVDFRAESYSPNSCKDDLGRLR

VGAAGTGADPTSRVEALVEAGDVIVVDVTAHGSAGVTVRRVVKQFQVQVIGGN

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ADGGIPFSGDMAKAGAGASTIMVSSLAGTEAEGVEFFQGRYKAYRNGSLGAM

AORTGADRFQDSKAGAEKLVPEGIEGRVPYKPGMGNIVHOMMGLRSLSSMGITGS

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BASE COUNT 854 a 505 c 681 g 838 t

ORIGIN

Query Match 100.0%; Score 9; DB 1; Length 2878;

Best Local Similarity 100.0%; Pred. No. 6.1e+03;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctgagtcga 9
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 Db 2157 TCTGAGTCA 2165

RESULT 10

AE000688/c

LOCUS AE000688 14801 bp DNA BCT 30-OCT-1997

DEFINITION Aquifex aeolicus section 20 of 109 of the complete genome.

ACCESSION AE000688

NID g2983063

KEYWORDS

SOURCE Aquifex aeolicus.

ORGANISM Aquifex aeolicus

Eubacteria; Aquificales; Aquificaceae; Aquifex.

REFERENCE 1 (bases 1 to 14801)

Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.,

Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aujay,M.,

Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.

The complete genome of the hyperthermophilic bacterium Aquifex

aeolicus

Nature 392 (6674), 353-358 (1998)

98196666

2 (bases 1 to 14801)

Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.,

Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aujay,M.,

Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.

Direct Submission

TITLE Submitted (25-JUL-1997) Diversa Corporation, Genomics, San Diego,

CA 92121

COMMENT Putative indicates no similarity to known proteins

Hypothetical indicates similarity to a protein of unknown function.

FEATURES Location/Qualifiers

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/strain="VF5"

/db_xref="taxon:63363"

335..883

/gene="aq_389"

335..883

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/transl_table=11

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/db_xref="PID:g2983080"

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903..1328

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903..1328

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/db_xref="PID:g2983070"

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DLKEIILENGVKYLNPKRIVIEKPFGLSKHAKDLNIIISVPKEEIEFRIDHVLG
KPOVONILAKFSNVSESVNLKCLVEKVEVIALEEVGVEGRKAYEKYGVIRDMON
HMLLSLIVWRLPDRAEDFHLKALKRAEFESLILGKYSQGRAPFALVKL
HFDDEETGVVFLATOKLKKLTVRCIHFKNPKIEERLLGCVPERNLLVFLYPE
QEVSRFNVISPLGFLCTESINRVSLKDLVGLPEIPEAYESLLIDVIRGDKTLFLDAE
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complement(13532..14434)
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/db_xref="PID:g2983136"
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YIAGSSAGHFAKVNHGIEYIGMEATAEGFELKKSPFDYDLREAVRVSQGSVIRSF
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/codon_start=1
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/db_xref="PID:g2983144"
/transl_table=11
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KFGPSYFERILQKVDLMDPLKAEKERENARKLEEVKIVLNQKAEELGITHSYEK
HKIVSYAFQKLYGKGVFLGEDYTVFDNLKQALQELTPEELGTQGT"
BASE COUNT 4017 a 3535 c 3230 g 4522 t
ORIGIN

Query Match 100.0%; Score 9; DB 1; Length 15304;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctgagtca 9
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Db 10724 TCTGAGTCA 10732

RESULT 12
AE000697/c 14150 bp DNA BCT 30-OCT-1997
LOCUS Aquifex aeolicus section 29 of 109 of the complete genome.
DEFINITION AE000697 AE000657
ACCESSION AE000697
NID 92983212

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KEYWORDS
SOURCE Aquifex aeolicus.
ORGANISM Aquifex aeolicus.
REFERENCE Eubacteria: Aquificales; Aquificaceae; Aquifex.
AUTHORS 1 (bases 1 to 14150)
Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.,
Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., AuJay,M.,
Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.
The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus
JOURNAL Nature 392 (6674), 353-358 (1998)
MEDLINE 98196666
REFERENCE 2 (bases 1 to 14150)
AUTHORS Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L.,
Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., AuJay,M.,
Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V.
Direct Submission
JOURNAL Submitted (25-JUL-1997) Diversa Corporation, Genomics, San Diego,
CA 92121
COMMENT Putative indicates no similarity to known proteins
Hypothetical indicates similarity to a protein of unknown function.
FEATURES
source
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/organism="Aquifex aeolicus"
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379..2496
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379..2496
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YRIPSYLHNVLIIINSQTPGYTLFTLLREYDLIAVNLNLIKISKKTLPAD
VEGVDQSINKLISKIQTSPSAVLDLGRKIMVDMANIEKRLDRVLDIELL
MSRTTPGEKKEKETTPRETEKVFYFNKRDLEIALSRLENFSGEVLNIDKDFN
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VYTLVSNVDEKELISYKNTPPATAENEGTLEKEKAFVFNNAIILKDYPERIKI
REKFKFLSEKPIKIKAKLVEVEKSELRLGELISWRTVFSKAYIPFWGGEATFRV
TPGQPQGLTFTFQNRNLNLEKFLAYEGRKNAVSEYITVNGEPAVISSGLE
FPVTEVSLSGIANVEPKYESIPVLTTPVLPDGNILLSVRLARQINSVQEPFVY
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ARKEAPEKNEVELFPVTCPHAPVTCSPNTLRMAKELADEVGLLHLHVAETKEVER
INEQKTPVSHLESIGFLDNKVLCAHWWTEKERELKERDVKIACHCESNLKLAS
GIAPVPDVKRGITVLTGDAANDNLNMLEETSTCAKFKHGNLDAKADAGTALK
IATENGFKVAGIKAGKVEEGEADLILVDTFDFEPFLYDPIFSQFVYSANSECIDTVI
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/notes="aq_589"
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isomerase/mannose-1-phosphate guany1 transferase"

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GKEEGVTELEKEPEEKPDYKAEVYSDGKHFWMCGIFLFLDRIVKDYQTLMPPIPF
HEWEDFIRKDFKNFEISDYAILERTKILAVKMDAGSDYGSWKAYDNLPDDEKR
NVLIGDKAMDSCSLSSGQNLKACIGLEDVFWVGTEADATLIVKRDYSQKKEIVF
ELEBEDNRAIEHVTSTPFGSITKLDGERYKIRKVVVKDKKEIPLRMHHRTVHFV
VLKGTAKRVKGDKEEFVHENSEFVPKSTPYKIINVGKIPLEMIEVQSGEYLGDDE
TLE"
gene      5161..6162
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CDS       5161..6162
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          /transl_table=11
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          /db_xref="PID:g2983218"
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LPNEETAQILNISKENYFEVKKLAGANKLYGALYVLLQSDSVKVNHRLLGIS
REAELEKAYANTGDFYRAHEILSEVGLPKNEIEKKCYRGLIRAAIALRFEKGN
PQSGANVQAALLDMANCPDNFRGINLGEIRAYLEVLGTEKIGNPPELLKYNKSEE"
6162..6235
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          6259..7572
CDS       /gene="aq_592"
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RVGENYLLYKGNKAGYKPLEVEKEIKKELVAKKQREKLEPAQEVFNKKEGE
VGKPLAFSSASLEETQRIIMVQKDLLNLVFGKEKVGYPYPSLAGYGLIVVKNRKE
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VALRAGVPLDMEFIQPHTGLAKTGILLSEACRGGEGYLLNKEGFRMFKRAPDME
LAPRDIYSRAETIEIRGRGVGEGARAYVYDLRLHGEKEIKERLPQVRQLAIDFEGV
DPAKELVIRPSAHYCMGGLIHENYKTSPTPLAGLVAGECACVSVHGARNLGGNSLT
ELVYFGICYGMAREFVETDPAVSESEPKSEETIEELMKREGNESLAQVRQNGE
ITWAKMGIFRDEKSLKAYDELSELRWNNIPVDKAKVFNNTNLVLELVLELNNLELA
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gene      complement(9580..10893)
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YDENRQKREILFARENLYXKISGAVGYTSPNPEVEKLEALBELGKIPASTQIVH
RDRHAQTLTLGLTIASSLEKFAEIRHQLETVLEVEPTKQGRGSSAMPHKKNPIH
SERICGLARTRANSIPAMEDVVLWHERDISHSVERVILPDSFIALDYTLNLFYELI
KGLVYNNRMRKNMELSGLYASSKILYLLTQKGLSDYAYDIVQRCAMKANWESDTKF
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11427..11623
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BROKDLTGKGLKPLTLREVSIGIHSTLSRIVNSKYVKTGVGTYSRTFFVRES
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RLEELKLLKRLTGR"
BASE COUNT 4344 a 2784 c 3074 g 3948 t
ORIGIN
Query Match 100.0%; Score 9; DB 1; Length 14150;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tctgagtc 9
Db 2254 TCTGAGTCA 2246
RESULT 13

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AE000723 15467 bp DNA BCT 30-OCT-1997
 LOCUS Aquifex aeolicus section 55 of 109 of the complete genome.
 DEFINITION
 ACCESSION AE000723 AE000657
 NID 92983569
 KEYWORDS
 SOURCE Aquifex aeolicus.
 ORGANISM Aquifex aeolicus.
 Eubacteria; Aquificales; Aquificaceae; Aquifex.
 REFERENCE
 AUTHORS Deckert, G., Warren, P.V., Gaasterland, T., Young, W.G., Lenox, A.L.,
 Graham, D.E., Overbeek, R., Snead, M.A., Keller, M., AuJay, M.,
 Huber, R., Feldman, R.A., Short, J.M., Olson, G.J., and Swanson, R.V.
 The complete genome of the hyperthermophilic bacterium Aquifex
 aeolicus
 JOURNAL Nature 392 (6674), 353-358 (1998)
 MEDLINE 98196666
 REFERENCE 2 (bases 1 to 15467)
 AUTHORS Deckert, G., Warren, P.V., Gaasterland, T., Young, W.G., Lenox, A.L.,
 Graham, D.E., Overbeek, R., Snead, M.A., Keller, M., AuJay, M.,
 Huber, R., Feldman, R.A., Short, J.M., Olson, G.J., and Swanson, R.V.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUL-1997) Diversa Corporation, Genomics, San Diego,
 CA 92121
 COMMENT Putative indicates no similarity to known proteins
 Hypothetical indicates similarity to a protein of unknown function.
 FEATURES
 source
 1..15467
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 PECFIIDEALAVGDAHQKCFRKLKHKQKGGIIFVSHDMNAVILCDRAILLHK
 EIEEGSPVTOAYVKLASLENKGIIFLQNGYGNFKAVIKVRLKSEHYTNNFP
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 IYRKDALEQVIKIFSSITDIOAKRLSKVASFNPVLYERKLFYLSILRVKEGOT
 GTHRVVQAQLCNLENTPKPRAPSTIVENGKVTYKAREFTKYLKIQTNLSDV
 PLLIREGDIYVLPDYPLLTLEAVKSGFFDYLFKFKTKTVFLVLDLIPKPEYFPR
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 PNVTYSKERKEIIQKVSKEPFFLMVSTLEPRKHGFQVLKAFELMKKGINVNLIVG
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 AILSMVAVIALILNEYITRKLKESNELLVRSNLFNALLNAEVVLAELKHMNLKY
 KWMFYSKLSAFEAEDRNFLSNLAFIRMAQSLMLGGLGVLAIKHETITGMVA
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 VAVVYTSKSDILATRYAEGSELLELHADNCGYTRMKGRELFKVAVSRSEVCRE
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 HTYAEETILGKINPRVGILSGIEEGKGNELVKETYPILLKATKLNFGNAGRDIIYAGT
 FDIIVCGFVGNVILKASESLGLAVVQMIKEIKRSILAKIGALLMLPNRFRKKAD

JOURNAL	J. Bacteriol. 179 (22), 7135-7155 (1997)
MEDLINE	98037514
REFERENCE	2 (bases 1 to 16071)
AUTHORS	Smith,D.R.
TITLE	Direct Submission
JOURNAL	Submitted (10-AUG-1997) Genomics and Technology Development, Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02154-8448, USA
FEATURES	Location/Qualifiers
source	1..16071
	/organism="Methanobacterium thermoautotrophicum"
	/strain="delta H"
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gene	85..531
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CDS	85..531
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gene	543..1121
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gene	1118..1768
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CDS	1118..1768
	/gene="MTH23"
	/note="Function Code:10.04 - Metabolism of Macromolecules, Ribosomal proteins; similar to, sp:LN:RSS_METJA AC:P54045, p()=1.1E-68, pid=58"
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	/db_xref="PID:g2621060"
	/translation="MIMFNMEWEPTQLGRLYKEGVITSIDEIFEFGHPIMELEIIL DALLPDLEEYIDVNLVQRMHSGKRVNFRIVAVGNKDGVLGCGKAREVGPALRK AVDDAKFNIIVKRGCGDWGCVGREHTVPFKVSKSGSVRVTLIPAPGGVLAIGDV CKTINRLAGIDVMSHTRGQQTIVNPARATFDALKQLSKVAKSERDLNGLVCSPI"
gene	1781..2239
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CDS	1781..2239
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	/product="ribosomal protein L7 (E.coli L30)"
	/db_xref="PID:g2621061"
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gene	2252..2692

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5529..6014
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CDS
5529..6014
/genes="MTH30"
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and interconversion ; similar to, pir:LN:H64381 AC:H64381,
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gene
6045..6272
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6045..6272
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Ribosomal proteins; similar to, sp:LN:R14E_METJA
AC:P54054, p()-5E-16, pid=51%"
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/product="ribosomal protein L14"
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gene
6287..7261
/genes="MTH32"
CDS
6287..7261
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Transcriptions--mRNA synthesis and modification (includes
regulators) ; similar to, pir:LN:E64318 AC:E64318,
p()-1.5E-94, pid=53%"
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/db_xref="PID:g2621069"
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968187-968101"
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7498..7947
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7498..7947

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/db_xref="PID:g2621070"
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GYDLNORIGYLSDEIELEAKINPAKYNIPSWMINRNDYETGEDKHLIESLEMC
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7964..8479
/genes="MTH35"
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7964..8479
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p()-2.1E-42, pid=51%"
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/db_xref="PID:g2621071"
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ETMVRRYRDARYLLGMASEHTKEREQLLGHVLTGLNEGAKLEDVLDITVEDVLR
RRLQTLVHKRGLARTVKEARQWVIHGHIALDGRKIDAPGYIVKRGEEKIGFYFSPM
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8497..8889
/genes="MTH36"
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8497..8889
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Ribosomal proteins; similar to, sp:LN:RS11_METJA
AC:P54021, p()-1.4E-13, pid=30%"
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/db_xref="PID:g2621072"
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ROESSPFAAMEAATRAADDAKEKGIIVGLHIKVRAPGGNGPRTPGPGAATRALARAG
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CDS
8891..9685
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Transcriptions--mRNA synthesis and modification (includes
regulators) ; similar to, gp:GI:e283852:gi707823,
p()-1.6E-35, pid=30%"
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/db_xref="PID:g2621073"
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PGVYVSGDLVSETPAKVPVYPIDPLVGLDDELEVAQLGVGRHAKWEPTTACA
YKYPRIESEDCECEICIEACPRDVLGESESGKVPVVDLENCMSCKSCVRACDKRAI
DVGVEGKFIETIDGSDVPDKVLLKACDILDRKAEQVITFCEGG"
gene
9689..10054
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Ribosomal proteins; similar to, sp:LN:R18E_METJA
AC:P54022, p()-2.2E-31, pid=52%"
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/db_xref="PID:g2621074"
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10056..10904
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/gene="MTH115"
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4550. .5119
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/db_xref="PID:g2621154"
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ILANIFGGRKKEPLMTSVTVGNLSSERIEPMKVPVTEEPDDADSKYRISTM
PSYILELPELDDIRFREKQORFAAYRFGKNSDMAQAIAELKEWLERNSIE
PSNFTIAQINHPVPGFLRKNELVKID"
5187. .5930
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5187. .5930
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similar to, pir:LN:G64472 AC:G64472, p()=2.8E-22, pid=25%"
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RNLVPRDAELIDANIIVTCINRESRSYLDTPIGLDELSEFLWATQGIIRIAGDTA
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MAASGKGVIFVNTGSLDKKTTFLRRANDNFSRYPAGIYSPYRLTSAVGRILIQP
NVDACGSEDCRVRVASEILRMLNETPEMLQKRGFRYNSKLIAIHSIDPARKAYIAD
GIYRDLRGLKSGYSYGPAPFLMYDTYMGPIRPIKRVGPSNAGSVKSTHAYILS
RREYRALADVNRMYRKYLKAPNYIRFRGIIGYRDLRIYSKITRTHTSKKMQLPFS
SVKV"
7097. .7273
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CDS
7097. .7273
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sp:LN:HEM2_STAAU AC:P50915, p()=0.017, pid=29%"
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/db_xref="PID:g2621157"
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RSNLKIKRERSE"
complement(7329. .8324)
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Histidine metabolism ; similar to, gp:GI:91001367,
p()=3.5E-10, pid=16%"
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DSKPPVQIRGLRGDGNEMVQIINSDGATEYIYAKGADLIYDNTQTGSSLRAGLKIID
TIMSSAGLYAGSPCTGCKLEKAEIMFKOLYGATKARNYFDVKFNIAHRADDVVVEFL
VRMYCDEPTVVRGREFSOVNVILDKSRPEMLEIKGFGASAIVRNVKQYIE"
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/gene="MTH120"
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to, sp:LN:MDAA_ECOLI AC:P17117, p()=3.7E-11, pid=24%"
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IPFSVILGYPAENPGTRDLDFDRIHLEKW"
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complement(9193. .9660)
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DNA replication--modification--repair--and recombination ;
similar to, sp:LN:MUTT_STRAM AC:P32091, p()=4.8E-11,
pid=25%"
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/db_xref="PID:g2621161"
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KIGTGESLEALKVEEENLEIPEEVGVVEQEPVINAHIILIRCRAGSVKLS
HEHGFAVWSDURRYLADWLSDFVFKLKEEDKEDSPGLGILFRMGVIL"
complement(9788. .10858)
/gene="MTH123"
CDS
complement(9788. .10858)
/gene="MTH123"
/note="Function Code:12.12 - Cell Processes, Broad
regulatory functions ; similar to, gp:GI:91652472
LN:P90905, p()=2.1E-31, pid=21%"
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/transl_table=11
/product="sensory transduction histidine kinase"
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EKANFLDKIRKNGAAYNWMNLNATYHFSGLDSRIVVYVSPSREDMIKIYHLA
EQYIPPAEIPPEHAESVEKELNELRLNELSAAQRELLKKNLSQRLNLEKEMIL
REINHRVNNMLIISILNQSRVYKDRDDMLFREQASRARAMHLERLYTSKGER
RVDFEYLRGLVRDLYHSFQDSGRIGLETIDDAELDINTVYPLALIVNEVETNAIK
HGFEGRGGIIRVSKRSDGGLLEIFDNGVGLPDPDPNSTMGTMCMLIRLSLEQMN
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complement(10314. .10404)
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81% ID to interval 747694"
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complement(10316. .10398)
/note="83 bp inverted repeat includes part of MTH123
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83% ID to interval 5546"
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83% ID to interval 8984"

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repeat_region complement(10316..10368)
/note="53 bp direct repeat includes part of MTH123
(sensory transduction histidine kinase - paralog.fam. 1);
87% ID to interval 408704"
repeat_region 10316..10397
/note="82 bp inverted repeat includes part of MTH123
(sensory transduction histidine kinase - paralog.fam. 1);
83% ID to interval 8984"
repeat_region 10316..10398
/note="83 bp inverted repeat includes part of MTH123
(sensory transduction histidine kinase - paralog.fam. 1);
83% ID to interval 5547"
repeat_region complement(10322..10404)
/note="83 bp direct repeat includes part of MTH123
(sensory transduction histidine kinase - paralog.fam. 1);
86% ID to interval 305884"
repeat_region complement(10346..10396)
/note="51 bp inverted repeat includes part of MTH123
(sensory transduction histidine kinase - paralog.fam. 1);
90% ID to interval 4001"
repeat_region 10346..10396
/note="51 bp inverted repeat includes part of MTH123
(sensory transduction histidine kinase - paralog.fam. 1);
90% ID to interval 4002"
BASE COUNT 2774 a 2581 c 2533 g 3044 t
ORIGIN

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Query Match 100.0%; Score 9; DB 1; Length 10932;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tctgagtcac 9
Db 1267 TCTGAGTCA 1259

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Search completed: June 24, 1999, 01:30:01
Job time: 2989 sec

